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		E	G	_	s					S	S	G	S	T		E
25	1898		_			-	•	_					_		_	_
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	1853															
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SEQ ID NO:6 and SEQ ID NO:7

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		s	R	P	A	E	D	G	N	A	I	R	R	R	R	I
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		C	P	D	C	G	G	R	F	T	T	F	E	R	V	Q
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	3019							_	_	-					_	gggc
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					G											
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		tcacgggccgtgctcgagggctcgatcatgaccaacaa S R A V L E A Q G S I M T N K
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65



SEQ ID NO:10 and SEQ ID NO:11

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SEO ID NO:12 and SEO ID NO:13

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PCT/US99/27318

SEQ ID NO:13 M A K I K P V H I L I V E A R 424 ttctatgacgatatggccgacgcgatgctcgatggagcgaaacat F Y D D M A D A M L D G A K H 469 gcgctggatgcggccggcgccacttatatattgtgcggtcccggg 5 ALDAAGATYILCGPG 514 qcactqqaaattcccgcgqcqatcgccatggcgctcgatggtgcc ALEIPAAIAMALDGA 559 gacgaaggcgggggggaatatgacggcttcgttgcgctcggcatg D E G G A E Y D G F V A L G M 10 604 gtgatccgcggcgagacctaccatttcgacatcgtcgccaacgag VIRGETYHFDIVANE 649 tecgegegegetgatggatetegeegteagegagageetggeg SARALMDLAVSESLA 694 ctcggcaacggcattctgacggtcgagaacgacgagcaggcctgg 15 LGNGILTVENDEQAW 739 gcacgggcccgccgtacggaaggcgacaagggcggattcgccgcg ARARRTEGDKGGFAA 784 cgcgccgccctgaccatgatcgaactgaagcaaagattgggcgca RAALTMIELKQRLGA 20 829 gagaagtga 837 E K * SEQ ID NO:14 ribCF 25 5'-GACGTTATTCCTGCTTGGGAG-3' SEQ ID NO:15 ribCR 5'-GATATTTTCGAGGATTACGAGAG -3' 30 SEQ ID NO:16 ribDF 5'-AAACATTCAGCTATCTCTCTCGT-3' **SEO ID NO:17** 35 ribDR 5'-TCTATCGCGATTTCTCCCATG-3' SEQ ID NO:18 glyAF 40 5'-CAGCCGTCCGATCACATATAG-3' SEQ ID NO:19 glyAR. 45 5'-AGTAGACCGGGACCTCTTCGG-3' SEQ ID NO:20 ribBAF 5'-GGCGGCTGAAGTAACTCCACT-3' 50 SEQ ID NO:21

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5'-AAGACGAGCTTCTCAAGACCT-3'

SEQ ID NO:22 ribHF
5'-ATGCCGATATCCTTGAGACCG-3'

SEQ ID NO:23 ribHR 5'-GTCTGCCCGGAGATAGGTGTC-3'

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